

# SEQUENCE LISTING

<110> Thulé, Peter M.  
 <120> GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION  
 <130> US 1292/01 (VA)  
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 <160> 6  
 <210> 1  
 <211> 51  
 <212> DNA  
 <213> Rattus norvegicus  
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 <223> STRANDEDNESS: double  
 TOPOLOGY: linear

<400> SEQ ID NO: 1

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51

<210> 2  
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 <213> Rattus norvegicus  
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 <223> STRANDEDNESS: double  
 TOPOLOGY: linear

<400> SEQ ID NO: 2

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 ccactgcccg ccgagacaca aaccagcga gcattgaaca ctgcacacgg ccatctgccc  
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60

120

180

219

<210> 3  
 <211> 270  
 <212> DNA  
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 <223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA  
 STRANDEDNESS: double  
 TOPOLOGY: both

<400> SEQ ID NO: 3

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gctg	ccgag	c	cagcc	cttca	taagg	ccctg	ggtat	ggcca	gccag	catg	g	tccact	gccc	180
g	ccgag	acac	aaaccc	agcg	agcatt	gaac	actgc	acacg	gccat	ctgc	cagag	agctg		240
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<210> 4  
 <211> 321  
 <212> DNA  
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 <223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA  
 STRANDEDNESS: double  
 TOPOLOGY: both

<400> SEQ ID NO: 4

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ggccag	agtc	cagga	accac	gggag	tgccc	cgtgc	gcccc	tg	tacaa	gc	aaaaca	aaact		120
tatttt	gaac	acggg	gatcc	tagca	gctg	cctg	acaat	catta	acccg	tgct	gccgag			180
ccagcc	cttc	ataag	gccct	gggtat	ggcc	agccag	catg	gtcc	actg	cc	cgccgag	acac		240
caaacc	cagc	gagcat	tga	ca	ctgc	acac	ggccat	ctgc	ccagag	agct	gtgacc	acca		300

cttccgctac tagctagccg c

321

<210> 5

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA

STRANDEDNESS: double

TOPOLOGY: both

<400> SEQ ID NO: 5

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ccaggaacca cgggagtgcc ccgtgcgccc atgtcacaag caaaacaaac ttattttgaa 180  
cacggggatc ctagcacgct gccctgacaa tcattaaccc gtgctgccga gccagccctt 240  
cataaggccc tgggtatggc cagccagcat ggtccactgc ccgccgagac acaaaccag 300  
cgagcattga aactgcaca cggccatctg cccagagagc tgtgaccacc acttccgcta 360  
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<210> 6

<211> 423

<212> DNA

<213> Artificial Sequence

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA

STRANDEDNESS: double

TOPOLOGY: both

<400> SEQ ID NO: 6

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acggggcact cccgtggttc ctggactctg gccccagtg tacatgggcg cacggggcac	120
tcccgtggtt cctggactct ggccccagt gtacatgggc gcacggggca ctcccgtggt	180
tcctggactc tggccccag tgtatcaca gcaaaacaaa cttattttga acacggggat	240
cctagcacgc tgccctgaca atcattaacc cgtgctgccg agccagccct tcataaggcc	300
ctgggtatgg ccagccagca tgggtccactg cccgccgaga cacaaacca gcgagcattg	360
aacactgcac acggccatct gccagagag ctgtgaccac cacttccgct actagctagc	420
cgc	423

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